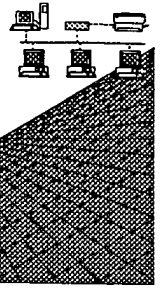


C. Karsman

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/157,289c

Art Unit / Team No. : 1646

Date Processed by STIC: 1/10/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/157,289C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 ✓ Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/157,289C

DATE: 01/10/2000

TIME: 13:24:18

Input Set: I157289C.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

PS

1 <110> APPLICANT: ASHKENAZI, AVI J
2 BOTSTEIN, DAVID
3 DODGE, KELLY H.
4 GURNEY, AUSTIN L.
5 KIM, KYUNG JIN
6 LAWRENCE, DAVID A.
7 PITTI, ROBERT
8 ROY, MARGARET A
9 TUMAS, DANIEL B
10 WOOD, WILLIAM I.
11 <120> TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
12 <130> FILE REFERENCE: P1134R2
13 <140> CURRENT APPLICATION NUMBER: US/09/157,289C
14 <141> CURRENT FILING DATE: 1998-09-18
15 <150> EARLIER APPLICATION NUMBER: US 60/059,288
16 <151> EARLIER FILING DATE: 1997-09-18
17 <150> EARLIER APPLICATION NUMBER: US 60/094,640
18 <151> EARLIER FILING DATE: 1998-07-30
19 <160> NUMBER OF SEQ ID NOS: 16
20 <210> SEQ ID NO 1
21 <211> LENGTH: 300
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
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26 1 5 10 15
27 Leu Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val
28 20 25 30
29 Ala Glu Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu
30 35 40 45
31 Arg Leu Val Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg
32 50 55 60
33 Pro Cys Arg Arg Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro
34 65 70 75
35 Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr
36 80 85 90
37 Cys Asn Val Leu Cys Gly Glu Arg Glu Glu Glu Ala Arg Ala Cys
38 95 100 105
39 His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly Phe Phe
40 110 115 120
41 Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro Gly
42 125 130 135
43 Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys
44 140 145 150

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/157,289C

DATE: 01/10/2000
TIME: 13:24:18

Input Set: I157289C.RAW

45	Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser
46					155					160					165
47	Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala
48					170					175					180
49	Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser
50					185					190					195
51	Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu
52					200					205					210
53	Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser
54					215					220					225
55	Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu
56					230					235					240
57	Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu
58					245					250					255
59	Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly
60					260					265					270
61	Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met
62					275					280					285
63	Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His
64					290					295					300

65 <210> SEQ ID NO 2

66 <211> LENGTH: 1114

67 <212> TYPE: DNA

68 <213> ORGANISM: Homo sapiens

69 <220> FEATURE:

70 <221> NAME/KEY: Unsure

71 <222> LOCATION: 1090

72 <223> OTHER INFORMATION: Unknown base

73 <400> SEQUENCE: 2

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76 atgagggcgc tggaggggcc aggcctgtcg ctgctgtgcc tgggtgtggc 150
77 gctgcctgcc ctgctgccgg tgcggctgt acgcggagtg gcagaaacac 200
78 ccacctacc cttggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
79 cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
80 cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag ttctggaact 350
81 acctggagcg ctgccgtac tgcaacgtcc tctgcgggga gcgtgaggag 400
82 gaggcacggg cttgccacgc caccacaac cgtgcctgcc gctgccgcac 450
83 cggcttcttc gcgcacgtg gtttctgtt ggagcacgca tcgtgtccac 500
84 ctggtgcggg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550
85 cagccgtgcc cccaggcac cttctcagcc agcagctcca gctcagagca 600
86 gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650
87 caggctcttc ctccatgac accctgtgca ccagctgcac tggcttcccc 700
88 ctcagcacca ggggtaccag agctgaggag tgtgagcgtg ccgtcatcga 750
89 ctttgtggct ttccaggaca tctccatcaa gaggctgcag cggctgtgc 800
90 aggccctcga ggccccggag ggctgggggtc cgacaccaag ggcggggcgc 850
91 gcggccttgc agctgaagct gcgtcggcgg ctcacggagc tcctgggggc 900
92 gcaggacggg gcgtgtgtg tgcggtgtg gcaggcgtg cgcgtggcca 950
93 ggatgcccgg gctggagcgg agcgtccgtg agcgttccct ccctgtgcac 1000
94 tgatcctggc cccctcttat ttattctaca tccttggcac cccacttgca 1050

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/157,289C

DATE: 01/10/2000
TIME: 13:24:18

Input Set: I157289C.RAW

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96 aaaaaaaaaa aaaa 1114
97 <210> SEQ ID NO 3
98 <211> LENGTH: 491
99 <212> TYPE: DNA
100 <213> ORGANISM: Unknown *see item 12 on Ena summary sheet*
101 <220> FEATURE:
102 <221> NAME/KEY: Unsure
103 <222> LOCATION: 62, 73, 86, 98
104 <223> OTHER INFORMATION: Unknown base
105 <400> SEQUENCE: 3
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W--> 107 cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgnng 100
108 ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgcct 150
109 gccgctgccg caccggttc ttgcgcacg ctggtttctg cttggagcac 200
110 gcatcgtgtc cacctggtgc cggcgtgatt gcccgggca ccccagcca 250
111 gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300
112 tccagctcag agcagtgccg gcccaccgc aactgcacgg ccctgggcct 350
113 ggccctcaat gtgccaggct cttcctccca tgacaccctg tgcaccagct 400
114 gactggtt cccctcagc accagggtac caggagctga ggagtgtgag 450
115 cgtgccgtca tcgacttgt ggctttccag gacatctcca t 491
116 <210> SEQ ID NO 4
117 <211> LENGTH: 73
118 <212> TYPE: DNA
119 <213> ORGANISM: Unknown
120 <220> FEATURE:
121 <221> NAME/KEY: Unsure
122 <222> LOCATION: 1-73
123 <223> OTHER INFORMATION: Organism - Unknown
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126 cattctgga ctacctggag cgc 73
127 <210> SEQ ID NO 5
128 <211> LENGTH: 271
129 <212> TYPE: DNA
130 <213> ORGANISM: Unknown
131 <220> FEATURE:
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133 <222> LOCATION: 1-271
134 <223> OTHER INFORMATION: Organism - Unknown
135 <220> FEATURE:
136 <221> NAME/KEY: Unsure
137 <222> LOCATION: 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233
138 <223> OTHER INFORMATION: Unknown base
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W--> 142 ggagcgtgag gaggaggcan gngcttgcca cgccaccac aaccgtgcct 150
W--> 143 gcnctgcag caccggttc ttgcgcacg ctgntttctg cttggagcac 200
W--> 144 gcatcgtgtc cacctggtgn cggcgtgatt gcnccgggca ccccagcca 250

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/157,289C

DATE: 01/10/2000
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Input Set: I157289C.RAW

145 gaacacgcat gcaaagccgt g 271
146 <210> SEQ ID NO 6
147 <211> LENGTH: 201
148 <212> TYPE: DNA
149 <213> ORGANISM: Unknown
150 <220> FEATURE:
151 <221> NAME/KEY: Unsure
152 <222> LOCATION: 1-201
153 <223> OTHER INFORMATION: Organism - Unknown
154 <220> FEATURE:
155 <221> NAME/KEY: Unsure
156 <222> LOCATION: 182
157 <223> OTHER INFORMATION: Unknown base
158 <400> SEQUENCE: 6
159 gcagttctgga aactacctgg agcgctgccg ctactgcaac gtcctctgcg 50
160 gggagcgtag ggaggaggca cgggcttgcc acgccacca caaccgtgcc 100
161 tgccgctgcc ccaccggctt cttcgcgcac gctggtttct gcttggagca 150
W--> 162 cgcatcgtgt ccacctgggtg ccggcgatgat tncgccgggc acccccagcc 200
163 a 201
164 <210> SEQ ID NO 7
165 <211> LENGTH: 277
166 <212> TYPE: DNA
167 <213> ORGANISM: Unknown
168 <220> FEATURE:
169 <221> NAME/KEY: Unsure
170 <222> LOCATION: 1-277
171 <223> OTHER INFORMATION: Organism - Unknown
172 <220> FEATURE:
173 <221> NAME/KEY: Unsure
174 <222> LOCATION: 142
175 <223> OTHER INFORMATION: Unknown base
176 <400> SEQUENCE: 7
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178 ggtcccagcc ttgcaccctg agctaggaca ccagttcccc tgaccctgtt 100
W--> 179 cttccctcct ggctgcaggc acccccagcc agaacacgca gnccagccgt 150
180 gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 200
181 ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250
182 ttcctcccat gacaccctgt gcaccag 277
183 <210> SEQ ID NO 8
184 <211> LENGTH: 199
185 <212> TYPE: DNA
186 <213> ORGANISM: Unknown
187 <220> FEATURE:
188 <221> NAME/KEY: Unsure
189 <222> LOCATION: 1-199
190 <223> OTHER INFORMATION: Organism - Unknown
191 <400> SEQUENCE: 8
192 gcatcgtgtc cacctgggtgc cggcgatgatt gccccgggca cccccagcca 50
193 gaacacgcag gcctagccgt gccccccagg caccttctca gccagcagct 100
194 ccagctcaga gcagtgccag cccccaccga actgcacggc cctgggcctg 150

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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/157,289C

 DATE: 01/10/2000
 TIME: 13:24:18

Input Set: I157289C.RAW

195 gccctcaatg tgccaggctc ttctctcccat gacaccctgt gcaccagct 199
 196 <210> SEQ ID NO 9
 197 <211> LENGTH: 226
 198 <212> TYPE: DNA
 199 <213> ORGANISM: Unknown
 200 <220> FEATURE:
 201 <221> NAME/KEY: Unsure
 202 <222> LOCATION: 1-226
 203 <223> OTHER INFORMATION: Organism - Unknown
 204 <220> FEATURE:
 205 <221> NAME/KEY: Unsure
 206 <222> LOCATION: 4, 9, 12, 165
 207 <223> OTHER INFORMATION: Unknown base
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 210 tgccagcccc accgcaactg cacggccctg ggcttggccc tcaatgtgcc 100
 211 aggctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150
 W- 212 tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200
 213 tttgtggctt tccaggacat ctccat 226
 214 <210> SEQ ID NO 10
 215 <211> LENGTH: 283
 216 <212> TYPE: DNA
 217 <213> ORGANISM: Homo sapiens
 218 <220> FEATURE:
 219 <221> NAME/KEY: Unsure
 220 <222> LOCATION: 1-283
 221 <223> OTHER INFORMATION: Organism - Unknown
 222 <220> FEATURE:
 223 <221> NAME/KEY: Unsure
 224 <222> LOCATION: 27, 64, 140
 225 <223> OTHER INFORMATION: Unknown base
 226 <400> SEQUENCE: 10
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 W- 228 cgcagtgccca gccntcccc caggcacctt ctcagccagc agtccagct 100
 W- 229 cagagcagtg ccagccccac cgcaactgca acgcccctggn ctggccctca 150
 230 atgtgccagg ctcttctctc catgacaccc tgtgcaccag ctgcactggc 200
 231 ttccccctca gcaccagggt accaggagct gaggagtgtg agcgtgccgt 250
 232 catcgacttt gtggctttcc aggacatctc cat 283
 233 <210> SEQ ID NO 11
 234 <211> LENGTH: 21
 235 <212> TYPE: DNA
 236 <213> ORGANISM: Unknown
 237 <220> FEATURE:
 238 <221> NAME/KEY: Unsure
 239 <222> LOCATION: 1-21
 240 <223> OTHER INFORMATION: Organism - Unknown
 241 <400> SEQUENCE: 11
 242 cacgctgggt tctgcttgga g 21
 243 <210> SEQ ID NO 12
 244 <211> LENGTH: 22

Input Set: I157289C.RAW

Line	?	Error/Warning	Original Text
95	W	"N" or "Xaa" used: Feature required	ctgaaagagg ctttttttta aatagaagaa atgaggtt
107	W	"N" or "Xaa" used: Feature required	cagttctgga antaactgga gcncgtccgc tactgnaa
140	W	"N" or "Xaa" used: Feature required	gccgagacag ccccacgacg tgtggcccgt gtccaccg
141	W	"N" or "Xaa" used: Feature required	cagttctgga antaactgga gcncgtccgc tactgnaa
142	W	"N" or "Xaa" used: Feature required	ggagcntgag gaggaggcan gngcttgcca cgccaccc
143	W	"N" or "Xaa" used: Feature required	gcngctgcag caccggnntt ttcgcgcacg ctgnnttc
144	W	"N" or "Xaa" used: Feature required	gcatcgtgtc cacctggtgn cggcgtgatt gcncgggg
162	W	"N" or "Xaa" used: Feature required	cgcacgtgtt ccacctggtg ccggcgtgat tnccccgg
179	W	"N" or "Xaa" used: Feature required	cttcctcctt ggctgcaggc acccccagcc agaacacg
209	W	"N" or "Xaa" used: Feature required	agcngtgcnc cncaggcacc ttctcagcca gcagttcc
212	W	"N" or "Xaa" used: Feature required	tcagcaccag ggtancagga gctgaggagt gtgagcgt
227	W	"N" or "Xaa" used: Feature required	cttgtccacc tggtgccggc gtgattnccc gggcaccc
228	W	"N" or "Xaa" used: Feature required	cgcagtgcca gccntcccc caggcacctt ctcagcca
229	W	"N" or "Xaa" used: Feature required	cagagcagtg ccagccccac cgcaactgca acgccttg